RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/553, 303_
Source: _PCT_
Date Processed by STIC: _10/25/ 2005_

ENTERED

PCT

<pre>
RAW SEQUENCE LISTING   DATE: 10/25/2005
PATENT APPLICATION: US/10/553,303   TIME: 10:35:10

Input Set : A:\Sequence listing - 12810-00153-US.txt
Output Set: N:\CRF4\10252005\J553303.raw
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<pre>
 3 <110> APPLICANT: Cirpus, Petra
 4   Oswald, Oliver
 5 ..   Ronne, Hans
 6   Dahlqvist, Anders
 7   Lenman, Marit
 8   Neal, Andrea
 9   Stahl, Ulf
10   Liu, Tao
11   Banas, Antoni
12   Wiberg, Eva
14 <120> TITLE OF INVENTION: USE OF GENES FOR INCREASING THE OIL CONTENT IN PLANTS
16 <130> FILE REFERENCE: 12810-00153-US
C--> 18 <140> CURRENT APPLICATION NUMBER: US/10/553,303
C--> 18 <141> CURRENT FILING DATE: 2005-10-14
18 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/003845
19 <151> PRIOR FILING DATE: 2004-04-13
21 <150> PRIOR APPLICATION NUMBER: EP 03008909.8
22 <151> PRIOR FILING DATE: 2003-04-16
24 <160> NUMBER OF SEQ ID NOS: 43
26 <170> SOFTWARE: PatentIn version 3.3
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 1146
30 <212> TYPE: DNA
31 <213> ORGANISM: Saccharomyces cerevisiae
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (1)..(1146)
37 <400> SEQUENCE: 1
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39 Met Ser Phe Arg Asp Val Leu Glu Arg Gly Asp Glu Phe Leu Glu Ala
40   1   5   10   15
42 tat ccc aga aga agc ccc ctt tgg aga ttt ctt tca tac agt aca tca   96
43 Tyr Pro Arg Arg Ser Pro Leu Trp Arg Phe Leu Ser Tyr Ser Thr Ser
44   20   25   30
46 tta ctg acc ttc ggt gta tca aaa ctg ctt ctt ttc aca tgc tat aat   144
47 Leu Leu Thr Phe Gly Val Ser Lys Leu Leu Leu Phe Thr Cys Tyr Asn
48   35   40   45
50 gtc aaa ttg aat ggt ttt gaa aaa tta gaa act gcc ttg gaa cgt tcc   192
51 Val Lys Leu Asn Gly Phe Glu Lys Leu Glu Thr Ala Leu Glu Arg Ser
52   50   55   60
54 aaa agg gaa aat aga ggc ctt atg acg gtc atg aac cat atg agt atg   240
55 Lys Arg Glu Asn Arg Gly Leu Met Thr Val Met Asn His Met Ser Met
56 65   70   75   80
</pre>

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58 gtc gat gat ccg tta gtt tgg gca aca cta cca tat aag tta ttt acg    288
59 Val Asp Asp Pro Leu Val Trp Ala Thr Leu Pro Tyr Lys Leu Phe Thr
60             85                  90                  95
62 tct ttg gac aac ata aga tgg tct ttg ggt gca cat aat att tgc ttt    336
63 Ser Leu Asp Asn Ile Arg Trp Ser Leu Gly Ala His Asn Ile Cys Phe
64            100                 105                 110
66 caa aat aaa ttt ctg gcc aac ttt ttc tca ctt ggc caa gtc ctt tca    384
67 Gln Asn Lys Phe Leu Ala Asn Phe Phe Ser Leu Gly Gln Val Leu Ser
68         115                 120                 125
70 aca gaa aga ttt ggg gtg ggc cca ttt caa ggt tct ata gat gct tca    432
71 Thr Glu Arg Phe Gly Val Gly Pro Phe Gln Gly Ser Ile Asp Ala Ser
72      130                 135                 140
74 ata aga ttg tta agc cct gac gac act tta gac ttg gaa tgg acc cct    480
75 Ile Arg Leu Leu Ser Pro Asp Asp Thr Leu Asp Leu Glu Trp Thr Pro
76 145                 150                 155                 160
78 cac tct gag gtc tct tct tcg cta aaa aaa gcc tac tcc ccg ccc ata    528
79 His Ser Glu Val Ser Ser Ser Leu Lys Lys Ala Tyr Ser Pro Pro Ile
80                 165                 170                 175
82 ata agg tcg aag cca tct tgg gtc cat gtt tat cca gaa gga ttt gta    576
83 Ile Arg Ser Lys Pro Ser Trp Val His Val Tyr Pro Glu Gly Phe Val
84             180                 185                 190
86 cta caa tta tat ccg cct ttt gaa aat tcg atg agg tat ttt aaa tgg    624
87 Leu Gln Leu Tyr Pro Pro Phe Glu Asn Ser Met Arg Tyr Phe Lys Trp
88         195                 200                 205
90 ggt att acc aga atg atc cta gaa gca aca aag ccg ccc att gta gta    672
91 Gly Ile Thr Arg Met Ile Leu Glu Ala Thr Lys Pro Pro Ile Val Val
92      210                 215                 220
94 cca ata ttt gct aca ggg ttt gaa aaa ata gca tcc gaa gca gtc aca    720
95 Pro Ile Phe Ala Thr Gly Phe Glu Lys Ile Ala Ser Glu Ala Val Thr
96 225                 230                 235                 240
98 gat tca atg ttt aga caa att cta cca aga aac ttt ggc tct gaa ata    768
99 Asp Ser Met Phe Arg Gln Ile Leu Pro Arg Asn Phe Gly Ser Glu Ile
100                245                 250                 255
102 aat gtt acc ata ggg gat cct tta aat gat gat tta atc gac agg tat   816
103 Asn Val Thr Ile Gly Asp Pro Leu Asn Asp Asp Leu Ile Asp Arg Tyr
104             260                 265                 270
106 aga aaa gaa tgg aca cat ttg gtt gaa aaa tac tat gat ccc aaa aat   864
107 Arg Lys Glu Trp Thr His Leu Val Glu Lys Tyr Tyr Asp Pro Lys Asn
108         275                 280                 285
110 cct aac gac ctc tct gac gaa ttg aaa tat ggt aaa gag gcg caa gat   912
111 Pro Asn Asp Leu Ser Asp Glu Leu Lys Tyr Gly Lys Glu Ala Gln Asp
112      290                 295                 300
114 tta aga agc aga tta gcc gct gaa ctg aga gcc cat gtt gct gaa att   960
115 Leu Arg Ser Arg Leu Ala Ala Glu Leu Arg Ala His Val Ala Glu Ile
116 305                 310                 315                 320
118 aga aat gaa gtt cgc aaa tta cca cgc gaa gac cct agg ttc aaa tcc   1008
120 Arg Asn Glu Val Arg Lys Leu Pro Arg Glu Asp Pro Arg Phe Lys Ser
121                 325                 330                 335
123 ccc tca tgg tgg aag cgg ttc aac acc acg gaa ggt aaa tcg gac cca   1056
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124 Pro Ser Trp Trp Lys Arg Phe Asn Thr Thr Glu Gly Lys Ser Asp Pro
125         340                 345                 350
127 gat gtt aaa gtc att ggc gaa aat tgg gca ata agg agg atg caa aag    1104
128 Asp Val Lys Val Ile Gly Glu Asn Trp Ala Ile Arg Arg Met Gln Lys
129         355                 360                 365
131 ttt ctg cct cca gag ggt aaa cca aag ggt aag gat gat tga            1146
132 Phe Leu Pro Pro Glu Gly Lys Pro Lys Gly Lys Asp Asp
133         370                 375                 380
136 <210> SEQ ID NO: 2
137 <211> LENGTH: 381
138 <212> TYPE: PRT
139 <213> ORGANISM: Saccharomyces cerevisiae
141 <400> SEQUENCE: 2
142 Met Ser Phe Arg Asp Val Leu Glu Arg Gly Asp Glu Phe Leu Glu Ala
143   1               5                 10                  15
144 Tyr Pro Arg Arg Ser Pro Leu Trp Arg Phe Leu Ser Tyr Ser Thr Ser
145         20                  25                  30
146 Leu Leu Thr Phe Gly Val Ser Lys Leu Leu Leu Phe Thr Cys Tyr Asn
147         35                  40                  45
148 Val Lys Leu Asn Gly Phe Glu Lys Leu Glu Thr Ala Leu Glu Arg Ser
149     50                  55                  60
150 Lys Arg Glu Asn Arg Gly Leu Met Thr Val Met Asn His Met Ser Met
151 65                  70                  75                  80
152 Val Asp Asp Pro Leu Val Trp Ala Thr Leu Pro Tyr Lys Leu Phe Thr
153             85                  90                  95
154 Ser Leu Asp Asn Ile Arg Trp Ser Leu Gly Ala His Asn Ile Cys Phe
155         100                 105                 110
156 Gln Asn Lys Phe Leu Ala Asn Phe Phe Ser Leu Gly Gln Val Leu Ser
157         115                 120                 125
158 Thr Glu Arg Phe Gly Val Gly Pro Phe Gln Gly Ser Ile Asp Ala Ser
159     130                 135                 140
160 Ile Arg Leu Leu Ser Pro Asp Asp Thr Leu Asp Leu Glu Trp Thr Pro
161 145                 150                 155                 160
162 His Ser Glu Val Ser Ser Ser Leu Lys Lys Ala Tyr Ser Pro Pro Ile
163             165                 170                 175
164 Ile Arg Ser Lys Pro Ser Trp Val His Val Tyr Pro Glu Gly Phe Val
165         180                 185                 190
166 Leu Gln Leu Tyr Pro Pro Phe Glu Asn Ser Met Arg Tyr Phe Lys Trp
167         195                 200                 205
169 Gly Ile Thr Arg Met Ile Leu Glu Ala Thr Lys Pro Pro Ile Val Val
170     210                 215                 220
171 Pro Ile Phe Ala Thr Gly Phe Glu Lys Ile Ala Ser Glu Ala Val Thr
172 225                 230                 235                 240
173 Asp Ser Met Phe Arg Gln Ile Leu Pro Arg Asn Phe Gly Ser Glu Ile
174             245                 250                 255
175 Asn Val Thr Ile Gly Asp Pro Leu Asn Asp Asp Leu Ile Asp Arg Tyr
176         260                 265                 270
177 Arg Lys Glu Trp Thr His Leu Val Glu Lys Tyr Tyr Asp Pro Lys Asn
178         275                 280                 285
```

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179 Pro Asn Asp Leu Ser Asp Glu Leu Lys Tyr Gly Lys Glu Ala Gln Asp
180     290             295             300
181 Leu Arg Ser Arg Leu Ala Ala Glu Leu Arg Ala His Val Ala Glu Ile
182 305             310             315                 320
183 Arg Asn Glu Val Arg Lys Leu Pro Arg Glu Asp Pro Arg Phe Lys Ser
184             325             330             335
185 Pro Ser Trp Trp Lys Arg Phe Asn Thr Thr Glu Gly Lys Ser Asp Pro
186             340             345             350
187 Asp Val Lys Val Ile Gly Glu Asn Trp Ala Ile Arg Arg Met Gln Lys
188             355             360             365
189 Phe Leu Pro Pro Glu Gly Lys Pro Lys Gly Lys Asp Asp
190     370             375             380
194 <210> SEQ ID NO: 3
195 <211> LENGTH: 1374
196 <212> TYPE: DNA
197 <213> ORGANISM: Arabidopsis thaliana
199 <220> FEATURE:
200 <221> NAME/KEY: CDS
201 <222> LOCATION: (5)..(1348)
203 <400> SEQUENCE: 3
204 caga atg gga att cat ttt gtt gac aag gca gat cta tgg aag agt gca   49
205      Met Gly Ile His Phe Val Asp Lys Ala Asp Leu Trp Lys Ser Ala
206       1               5                  10                  15
208 ctg ttg ttc aat ctt aaa ctt cgt gat cga ttt cga atc gcc gtc gat   97
209 Leu Leu Phe Asn Leu Lys Leu Arg Asp Arg Phe Arg Ile Ala Val Asp
210             20                  25                  30
212 gat cac cgt ggt cga gct acg gtt ttc tca ccg gat ggt tgc ttc tct  145
213 Asp His Arg Gly Arg Ala Thr Val Phe Ser Pro Asp Gly Cys Phe Ser
214             35                  40                  45
216 tcc act atc cac cgc tgg gtg act cga ttc cgg aac ttt cgc cgg gag  193
217 Ser Thr Ile His Arg Trp Val Thr Arg Phe Arg Asn Phe Arg Arg Glu
218             50                  55                  60
220 tct ctc cct tct cca ccg gct ttt tat cgc aga cga gtt tct aag gac  241
221 Ser Leu Pro Ser Pro Pro Ala Phe Tyr Arg Arg Arg Val Ser Lys Asp
222     65                  70                  75
224 tta acg gca gaa gaa gag tct gct ctt ttc cgg atg cta caa act gtg  289
225 Leu Thr Ala Glu Glu Glu Ser Ala Leu Phe Arg Met Leu Gln Thr Val
226  80                  85                  90                  95
228 gct gtt ccc ctt att gga aat gct tgt cat gtt ttc atg aat ggt ttt  337
229 Ala Val Pro Leu Ile Gly Asn Ala Cys His Val Phe Met Asn Gly Phe
230             100             105             110
232 aac cgt gtt cag gta tat ggt tta gag aaa ttg cat gat gct tta ctc  385
233 Asn Arg Val Gln Val Tyr Gly Leu Glu Lys Leu His Asp Ala Leu Leu
234             115             120             125
236 aac aga cca aag aac aag cct ctt gta acg gtg agc aat cat gtt gca  433
237 Asn Arg Pro Lys Asn Lys Pro Leu Val Thr Val Ser Asn His Val Ala
238             130             135             140
240 tct gtg gat gat cca ttt gtc att gct tca tta ctt cca cct aaa ttt  481
241 Ser Val Asp Asp Pro Phe Val Ile Ala Ser Leu Leu Pro Pro Lys Phe
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Input Set : A:\Sequence listing - 12810-00153-US.txt
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242     145                   150                   155
244 cta ctt gat gcc cgt aat ttg agg tgg acg ctc tgt gct aca gat aga   529
245 Leu Leu Asp Ala Arg Asn Leu Arg Trp Thr Leu Cys Ala Thr Asp Arg
246 160                   165                   170                   175
248 tgc ttt aaa aac cct gta act tca gct ttc tct cga tct gtc aaa gtt   577
249 Cys Phe Lys Asn Pro Val Thr Ser Ala Phe Ser Arg Ser Val Lys Val
250                   180                   185                   190
252 ttg cca att tct cgt ggt gaa gga att tat cag cag gga atg gac att   625
253 Leu Pro Ile Ser Arg Gly Glu Gly Ile Tyr Gln Gln Gly Met Asp Ile
254                   195                   200                   205
256 gcg att tcg aaa ttg aac aac gga ggg tgg gtt cac atc ttt cca gaa   673
257 Ala Ile Ser Lys Leu Asn Asn Gly Gly Trp Val His Ile Phe Pro Glu
258             210                   215                   220
260 ggc agt cgc tcc cgg gat ggt gga aag act atg ggc tca gcg aag agg   721
261 Gly Ser Arg Ser Arg Asp Gly Gly Lys Thr Met Gly Ser Ala Lys Arg
262     225                   230                   235
264 ggt atc gga agg ttg att ttg gac gca gat act ctc cct atg gtt gtt   769
265 Gly Ile Gly Arg Leu Ile Leu Asp Ala Asp Thr Leu Pro Met Val Val
266 240                   245                   250                   255
268 cct ttt gtg cat act ggt atg cag gat ata atg cca gtt gga gct agt   817
269 Pro Phe Val His Thr Gly Met Gln Asp Ile Met Pro Val Gly Ala Ser
270                   260                   265                   270
272 gtt cca cgg att ggc aag aca gtg aca gtg atc att gga gac cct att   865
273 Val Pro Arg Ile Gly Lys Thr Val Thr Val Ile Ile Gly Asp Pro Ile
274             275                   280                   285
276 cat ttt aat gac att ctc agc act gaa gga gcc caa cac gtc tca agg   913
277 His Phe Asn Asp Ile Leu Ser Thr Glu Gly Ala Gln His Val Ser Arg
278             290                   295                   300
280 aaa cac ctg tat gac gcc gtt tcg tcc aga att gga caa aga ctg tac   961
281 Lys His Leu Tyr Asp Ala Val Ser Ser Arg Ile Gly Gln Arg Leu Tyr
282     305                   310                   315
284 gat tta aaa gca caa gtt gat aga gta tat ata gaa caa caa tct atg   1009
285 Asp Leu Lys Ala Gln Val Asp Arg Val Tyr Ile Glu Gln Gln Ser Met
286 320                   325                   330                   335
288 atg tca cac aat gcc aaa aca ccc tcg gac cgt gct gct gag atc ttt   1057
289 Met Ser His Asn Ala Lys Thr Pro Ser Asp Arg Ala Ala Glu Ile Phe
290             340                   345                   350
292 cat aga gtc gat tgg gac tca ttt ggg atg gga gca caa ttt tca gaa   1105
293 His Arg Val Asp Trp Asp Ser Phe Gly Met Gly Ala Gln Phe Ser Glu
294             355                   360                   365
296 gaa tca tca ccc agt agt aaa ccg att ggc caa agc gat gat cgc att   1153
297 Glu Ser Ser Pro Ser Ser Lys Pro Ile Gly Gln Ser Asp Asp Arg Ile
298             370                   375                   380
300 gtc aga tct ccc aaa agg aga gtc tca ccc gaa gga ggg gtc agc ttg   1201
301 Val Arg Ser Pro Lys Arg Arg Val Ser Pro Glu Gly Gly Val Ser Leu
302     385                   390                   395
304 aag att aag aag ctc atg gac tca acc gag atg atg ggg ttt gcg gct   1249
305 Lys Ile Lys Lys Leu Met Asp Ser Thr Glu Met Met Gly Phe Ala Ala
306 400                   405                   410                   415
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/25/2005
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Input Set : A:\Sequence listing - 12810-00153-US.txt
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; N Pos. 423
Seq#:16; N Pos. 385,412
Seq#:17; N Pos. 410
Seq#:18; N Pos. 420
Seq#:19; N Pos. 397
Seq#:23; N Pos. 423
Seq#:29; N Pos. 467
Seq#:31; N Pos. 26
Seq#:33; N Pos. 432
Seq#:34; N Pos. 216
Seq#:35; N Pos. 432

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:7; Line(s) 571
Seq#:8; Line(s) 596
Seq#:9; Line(s) 617
Seq#:10; Line(s) 637
Seq#:11; Line(s) 657
Seq#:12; Line(s) 677
Seq#:13; Line(s) 697
Seq#:14; Line(s) 718
Seq#:15; Line(s) 738
Seq#:16; Line(s) 764
Seq#:17; Line(s) 789
Seq#:18; Line(s) 814
Seq#:19; Line(s) 839
Seq#:20; Line(s) 861
Seq#:21; Line(s) 881
Seq#:22; Line(s) 902
Seq#:23; Line(s) 928
Seq#:24; Line(s) 949
Seq#:25; Line(s) 969
Seq#:26; Line(s) 989
Seq#:27; Line(s) 1009
Seq#:28; Line(s) 1030
Seq#:29; Line(s) 1055
Seq#:30; Line(s) 1076
Seq#:31; Line(s) 1102
Seq#:32; Line(s) 1122
Seq#:33; Line(s) 1147
Seq#:34; Line(s) 1173

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/25/2005
PATENT APPLICATION: US/10/553,303   TIME: 10:35:11

Input Set : A:\Sequence listing - 12810-00153-US.txt
Output Set: N:\CRF4\10252005\J553303.raw

Seq#:35; Line(s) 1199

VERIFICATION SUMMARY   DATE: 10/25/2005

PATENT APPLICATION: **US/10/553,303**   TIME: 10:35:11

Input Set : **A:\Sequence listing - 12810-00153-US.txt**

Output Set: **N:\CRF4\10252005\J553303.raw**

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L:18 M:270 C: Current Application Number differs, Replaced Current Application No
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:606 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:420
L:773 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:360
L:798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:360
L:823 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:360
L:848 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:360
L:938 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:420
L:1065 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:420
L:1105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
L:1157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:420
L:1179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:180
L:1209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:420
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